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Date: 28 April 2004

Please Deliver to:

Examiner Maryam Monshipouri
Art Unit 1652**Faxed to: 1-571-273-0932****Faxed to: 1-703-872-9306****Re: 09/854,731****From: J. Kenneth Joung****Fax: (302) 892-1026****Phone: (302) 992-4929****Pages: 4 (including cover)**

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Examiner Monshipouri:

Pursuant to our telephone conversation on Friday, April 23, 2004, please find enclosed the sequence alignment and percent identity comparisons that you requested.

Please call me at 302-992-4929 if you have any questions.

Respectfully submitted,**J KENNETH JOUNG**
Attorney for Applicants
Reg. No. 41, 881

Appendix A

Alignment of the amino acid sequences of: 1) SEQ ID NO:4 of the instant application, 2) Accession No. T03023 (NCBI Database General Identifier No. 7446431) and 3) Accession No. T02033 (NCBI Database General Identifier No. 7446432). The alignment was performed using default parameters of the Clustal V algorithm of the MegAlign program in the DNASTar suite. The percent identity is shown in Appendix B, included herewith. The program uses dashes to maximize the alignment.

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      10      20      30      40      50      60
-----+-----+-----+-----+-----+
1 MGQCYGK--GASGRTADDEGGVVTEHQSPPPANGLPSTPPRQQAQQAQQVGTTPRRRGSK SEQ ID NO:4
1 MGQCYGKAGGASSRRADHD-----DAVAP-----PSPLPANGAPTTPPQQPATPGRR--K T03023
1 MGQCYGKARGASSR-ADHDADPSGAGSVAP-----PSPLPANGAPLP----ATPRRH--K T02033

      70      80      90     100     110     120
-----+-----+-----+-----+-----+
59 SGSTTPGHQ----TPGVA-WPSPYPSSGGASPLPAGVSPSPARSTPRRFFKRPFPPPPSPAK SEQ ID NO:4
48 SGSATPVHHQAATT---AWPSPYPAGGASPLPAGVSPSPARSTPRRFFKRPFPPPPSPAK T03023
49 SGSTTPVHHQAATPGAAAWPSPYPAGGASPLPAGVSPSPARSTPRRFFKRPFPPPPSPAK T02033

      HIKATLAKRLGGGKPKEGTIPKEGGAGAGXGXG-----GAADSABAEERPLDKTFGPAK Majority
-----+-----+-----+-----+-----+
      130     140     150     160     170     180
-----+-----+-----+-----+-----+
114 HIKATLAKRLGGGKPKEGTIPKEGGVGAGGGGG-----GAADGAETERPLDKTFGFSK SEQ ID NO:4
104 HIKATLAKRLGGGKPKEGTIPKEGGAGV-----AADSABAEERPLDKTFGPAN T03023
109 HIKATLAKRLGGGKPKEGTIPKEGGAGAGAGAGAGAGAAGAAGAAADSABADRPLDKTFGPAK T02033

      190     200     210     220     230     240
-----+-----+-----+-----+-----+
167 NFGAKYELGKEVGRGHFGHTCSAVVKKGEYKGQTVAVKIIAKAKMTTAISIEDVRREVKI SEQ ID NO:4
151 NFGAKYDLGKEVGRGHFGHTCSALVKKGEYKGHAVAVKIIISKAKMTTAISIEDVRREVKI T03023
169 NFGAKYDLGKEVGRGHFGHTCSAVVKKGEHKGHTVAVKIIISKAKMTTAISIEDVRREVKI T02033

      250     260     270     280     290     300
-----+-----+-----+-----+-----+
227 LRALSGHNNLVKIFYDACEGLNVYIVMELCEGGELLDRILARGGRYTEEDAKAIVVQILS SEQ ID NO:4
211 LKALSGHNNLVKIFYDACEGLNVYIVMELCEGGELLDRILARGGRYTEVDAKAIIVVQILS T03023
229 LKALSGHNNLVRFYDACEGLNVYIVMELCEGGELLDRILARGGRYTEEDAKAIIVQILS T02033

      310     320     330     340     350     360
-----+-----+-----+-----+-----+
287 VVAFCHLQGVVHRDLKPENFLFTTRDENAPMKLIDFGLSDFIRPDERLNDIVGSAYYVAP SEQ ID NO:4
271 VVSFCHLQGVVHRDLKPENFLPATRDESAPMKLIDFGLSDFIRPDERLNDIVGSVYYVAP T03023
289 VVAFCHLQGVVHRDLKPENFLFTTRDESAPMKLIDFGLSDFIRPDERLNDIVGSAYYVAP T02033

      370     380     390     400     410     420
-----+-----+-----+-----+-----+
347 EVLHRSYSMEADIWSIGVITYILLCGSRPFWARTESGIFRSVLRADPNFDDSPWPVTSAB SEQ ID NO:4
331 EVLHRSYSMEADIWSIGVITYILLCGSRPFWARTESGIFRSVLRADPNFDDSPWPSVSAE T03023
349 EVLHRSYSMEADIWSIGVITYILLCGSRPFWARTESGIFRSVLRADPNFDDSPWPSVSAE T02033
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      430      440      450      460      470      480
-----+-----+-----+-----+-----+
407 AKDFVKRFLNKDYRKRMTAVQALTHPWLRDEQRQIPLDILIFRLIKQYLRATPLKRLALK SEQ ID NO:4
391 AKDFVKRFLNKDYRKRMTAVQALTHPWLRDEQRQIPLDILVFRLVKQYLRATPLKRLALK T03023
409 AKDFVKRFLNKDYRKRMTAVQALTHPWLRDEQRQIPLDILIFRLVKQYLRATPLKRLALK T02033

      490      500      510      520      530      540
-----+-----+-----+-----+-----+
467 ALSKALREDELLYLKLQFKLLEPRDGFVSLDNFRTALTRYLTDAMKESRVLEFLHALEPL SEQ ID NO:4
451 ALSKALREDELLYLRLQFKLLEPRDGLVSLDNFRTALTRYVTDAMRESRVLEFLHALDPL T03023
469 ALSKALSEDELLYLRLQFKLLEPRDGFVSLDNFRTALTRYSTDAMRESRVLEBPQHALBPL T02033

      550      560      570      580      590      600
-----+-----+-----+-----+-----+
527 AYRRMDFEEFCAAAISPYQLEALERWEEIAGTAFQHFQEGNRVISVEELAQELNLAPTH SEQ ID NO:4
511 AYRKMDLEEFCAAAISPYQLEALESWEEIAGTAFQHFQEGNRVISVEELAQELNLAPTH T03023
529 AYRKMDFEFCAAAISPYQLEALERWEEIAGTAFQHFQEGNRVISVEELAQELNLAPTH T02033

      610      620      630
-----+-----+-----+
587 YSIVQDWIRKSDGKLNFLGFTKFLHGVTTIRGSNTRRH SEQ ID NO:4
571 YSIVQDWIRKSDGKLNFLGFTKFLHGVTTIRGSNTRRH T03023
589 YSIVQDWIRKSDGKLNFLGFTKFLHGVTTIRGSNTRRH T02033

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BB1171 US DIV, Application No. 09/854,731

Appendix B

Calculation of the percent sequence identities of: 1) SEQ ID NO:4 of the instant application, 2) Accession No. T03023 (NCBI Database General Identifier No. 7446431) and 3) Accession No. T02033 (NCBI Database General Identifier No. 7446432). In the chart below the percent similarity is shown in the upper triangle and the percent divergence is shown in the lower triangle.

	SEQ ID NO:4	T03023	T02033	
SEQ ID NO:4	***	87.8	86.7	SEQ ID NO:4
T03023	9.6	***	91.6	T03023
T02033	9.2	5.3	***	T02033
	SEQ ID NO:4	T03023	T02033	